

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: DIXIT, VISHA M.
- (ii) TITLE OF INVENTION: CD40 BINDING COMPOSITIONS AND METHODS OF USING SAME
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: MORRISON & FOERSTER
  - (B) STREET: 755 Page Mill Road
  - (C) CITY: Palo Alto
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: KONSKI, ANTOINETTE F.
  - (B) REGISTRATION NUMBER: 34,202
  - (C) REFERENCE/DOCKET NUMBER: 203442102500
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (415) 813-5600
  - (B) TELEFAX: (415) 494-0792
  - (C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 211..1911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGAAGGCCA CGCGCCCGGC GCCCCTGAGC CGGCCGAGCG GCGACGGACC GCGAGATGAG	60
GAAAATGAGG CCCAAAGAAG TGATGCCACT TGGTTAAGGT CCCAGAGCAG GTCAGAATCA	120
GACCTAGGAT CAGAAACCTG GCTCCTGGCT CCTGCTCCCT ACTCTTCTAA GGATCGCTGT	180
CCTGACAGAA GAGAACTCCT CTTTCCTAAA ATG GAG TCG AGT AAA AAG ATG GAC	234
Met Glu Ser Ser Lys Lys Met Asp	

1								5								
TCT	CCT	GGC	GCG	CTG	CAG	ACT	AAC	CCG	CCG	CTA	AAG	CTG	CAC	ACT	GAC	282
Ser	Pro	Gly	Ala	Leu	Gln	Thr	Asn	Pro	Pro	Leu	Lys	Leu	His	Thr	Asp	
10				15				20								
CGC	AGT	GCT	GGG	ACG	CCA	GTT	TTT	GTC	CCT	GAA	CAA	GGA	GGT	TAC	AAG	330
Arg	Ser	Ala	Gly	Thr	Pro	Val	Phe	Val	Pro	Glu	Gln	Gly	Gly	Tyr	Lys	
25				30				35				40				
GAA	AAG	TTT	GTG	AAG	ACC	GTG	GAG	GAC	AAG	TAC	AAG	TGT	GAG	AAG	TGC	378
Glu	Lys	Phe	Val	Lys	Thr	Val	Glu	Asp	Lys	Tyr	Lys	Cys	Glu	Lys	Cys	
45				50				55								
CAC	CTG	GTG	CTG	TGC	AGC	CCG	AAG	CAG	ACC	GAG	TGT	GGG	CAC	CGC	TTC	426
His	Leu	Val	Leu	Cys	Ser	Pro	Lys	Gln	Thr	Glu	Cys	Gly	His	Arg	Phe	
60				65				70								
TGC	GAG	AGC	TGC	ATG	GCG	GCC	CTG	CTG	AGC	TCT	TCA	AGT	CCA	AAA	TGT	474
Cys	Glu	Ser	Cys	Met	Ala	Ala	Leu	Leu	Ser	Ser	Ser	Ser	Pro	Lys	Cys	
75				80				85								
ACA	GCG	TGT	CAA	GAG	AGC	ATC	GTT	AAA	GAT	AAG	GTG	TTT	AAG	GAT	AAT	522
Thr	Ala	Cys	Gln	Glu	Ser	Ile	Val	Lys	Asp	Lys	Val	Phe	Lys	Asp	Asn	
90				95				100								
TGC	TGC	AAG	AGA	GAA	ATT	CTG	GCT	CTT	CAG	ATC	TAT	TGT	CGG	AAT	GAA	570
Cys	Cys	Lys	Arg	Glu	Ile	Leu	Ala	Leu	Gln	Ile	Tyr	Cys	Arg	Asn	Glu	
105				110				115				120				
AGC	AGA	GGT	TGT	GCA	GAG	CAG	TTA	ATG	CTG	GGA	CAT	CTG	GTG	CAT	TTA	618
Ser	Arg	Gly	Cys	Ala	Glu	Gln	Leu	Met	Leu	Gly	His	Leu	Val	His	Leu	
125				130				135								
AAA	AAT	GAT	TGC	CAT	TTT	GAA	GAA	CTT	CCA	TGT	GTG	CGT	CCT	GAC	TGC	666
Lys	Asn	Asp	Cys	His	Phe	Glu	Glu	Leu	Pro	Cys	Val	Arg	Pro	Asp	Cys	
140				145				150								
AAA	GAA	AAG	GTC	TTG	AGG	AAA	GAC	CTG	CGA	GAC	CAC	GTG	GAG	AAG	GCG	714
Lys	Glu	Lys	Val	Leu	Arg	Lys	Asp	Leu	Arg	Asp	His	Val	Glu	Lys	Ala	
155				160				165								
TGT	AAA	TAC	CGG	GAA	GCC	ACA	TGC	AGC	CAC	TGC	AAG	AGT	CAG	GTT	CCG	762
Cys	Lys	Tyr	Arg	Glu	Ala	Thr	Cys	Ser	His	Cys	Lys	Ser	Gln	Val	Pro	
170				175				180								
ATG	ATC	GCG	CTG	CAG	AAA	CAC	GAA	GAC	ACC	GAC	TGT	CCC	TGC	GTG	GTG	810
Met	Ile	Ala	Leu	Gln	Lys	His	Glu	Asp	Thr	Asp	Cys	Pro	Cys	Val	Val	
185				190				195				200				
GTG	TCC	TGC	CCT	CAC	AAG	TGC	AGC	GTC	CAG	ACT	CTC	CTG	AGG	AGC	GAG	858
Val	Ser	Cys	Pro	His	Lys	Cys	Ser	Val	Gln	Thr	Leu	Leu	Arg	Ser	Glu	
205				210				215								
TTG	AGT	GCA	CAC	TTG	TCA	GAG	TGT	GTC	AAT	GCC	CCC	AGC	ACC	TGT	AGT	906
Leu	Ser	Ala	His	Leu	Ser	Glu	Cys	Val	Asn	Ala	Pro	Ser	Thr	Cys	Ser	
220				225				230								
TTT	AAG	CGC	TAT	GGC	TGC	GTT	TTT	CAG	GGG	ACA	AAC	CAG	CAG	ATC	AAG	954
Phe	Lys	Arg	Tyr	Gly	Cys	Val	Phe	Gln	Gly	Thr	Asn	Gln	Gln	Ile	Lys	
235				240				245								
GCC	CAC	GAG	GCC	AGC	TCC	GCC	GTG	CAG	CAC	GTC	AAC	CTG	CTG	AAG	GAG	1002

Ala	His	Glu	Ala	Ser	Ser	Ala	Val	Gln	His	Val	Asn	Leu	Leu	Lys	Glu		
250						255					260						
TGG	AGC	AAC	TCG	CTC	GAA	AAG	AAG	GTT	TCC	TTG	TTG	CAG	AAT	GAA	AGT	1050	
Trp	Ser	Asn	Ser	Leu	Glu	Lys	Lys	Val	Ser	Leu	Leu	Gln	Asn	Glu	Ser		
265					270					275					280		
GTA	GAA	AAA	AAC	AAG	AGC	ATA	CAA	AGT	TTG	CAC	AAT	CAG	ATA	TGT	AGC	1098	
Val	Glu	Lys	Asn	Lys	Ser	Ile	Gln	Ser	Leu	His	Asn	Gln	Ile	Cys	Ser		
				285					290					295			
TTT	GAA	ATT	GAA	ATT	GAG	AGA	CAA	AAG	GAA	ATG	CTT	CGA	AAT	AAT	GAA	1146	
Phe	Glu	Ile		Ile	Glu	Arg	Gln	Lys	Glu	Met	Leu	Arg	Asn	Asn	Glu		
			300					305					310				
TCC	AAA	ATC	CTT	CAT	TTA	CAG	CGA	GTG	ATA	GAC	AGC	CAA	GCA	GAG	AAA	1194	
Ser	Lys	Ile	Leu	His	Leu	Gln	Arg	Val	Ile	Asp	Ser	Gln	Ala	Glu	Lys		
		315					320					325					
CTG	AAG	GAG	CTT	GAC	AAG	GAG	ATC	CGG	CCC	TTC	CGG	CAG	AAC	TGG	GAG	1242	
Leu	Lys	Glu	Leu	Asp	Lys	Glu	Ile	Arg	Pro	Phe	Arg	Gln	Asn	Trp	Glu		
	330					335					340						
GAA	GCA	GAC	AGC	ATG	AAG	AGC	AGC	GTG	GAG	TCC	CTC	CAG	AAC	CGC	GTG	1290	
Glu	Ala	Asp	Ser	Met	Lys	Ser	Ser	Val	Glu	Ser	Leu	Gln	Asn	Arg	Val		
345					350					355					360		
ACC	GAG	CTG	GAG	AGC	GTG	GAC	AAG	AGC	GCG	GGG	CAA	GTG	GCT	CGG	AAC	1338	
Thr	Glu	Leu	Glu	Ser	Val	Asp	Lys	Ser	Ala	Gly	Gln	Val	Ala	Arg	Asn		
				365					370					375			
ACA	GGC	CTG	CTG	GAG	TCC	CAG	CTG	AGC	CGG	CAT	GAC	CAG	ATG	CTG	AGT	1386	
Thr	Gly	Leu	Leu	Glu	Ser	Gln	Leu	Ser	Arg	His	Asp	Gln	Met	Leu	Ser		
			380					385					390				
GTG	CAC	GAC	ATC	CGC	CTA	GCC	GAC	ATG	GAC	CTG	GGC	TTC	CAG	GTC	CTG	1434	
Val	His	Asp	Ile	Arg	Leu	Ala	Asp	Met	Asp	Leu	Gly	Phe	Gln	Val	Leu		
		395				400						405					
GAG	ACC	GCC	AGC	TAC	AAT	GGA	GTG	CTC	ATC	TGG	AAG	ATT	CGC	GAC	TAC	1482	
Glu	Thr	Ala	Ser	Tyr	Asn	Gly	Val	Leu	Ile	Trp	Lys	Ile	Arg	Asp	Tyr		
	410				415						420						
AAG	CGG	CGG	AAG	CAG	GAG	GCC	GTC	ATG	GGG	AAG	ACC	CTG	TCC	CTT	TAC	1530	
Lys	Arg	Arg	Lys	Gln	Glu	Ala	Val	Met	Gly	Lys	Thr	Leu	Ser	Leu	Tyr		
425					430					435					440		
AGC	CAG	CCT	TTC	TAC	ACT	GGT	TAC	TTT	GGC	TAT	AAG	ATG	TGT	GCC	AGG	1578	
Ser	Gln	Pro	Phe	Tyr	Thr	Gly	Tyr	Phe	Gly	Tyr	Lys	Met	Cys	Ala	Arg		
				445					450					455			
GTC	TAC	CTG	AAC	GGG	GAC	GGG	ATG	GGG	AAG	GGG	ACG	CAC	TTG	TCG	CTG	1626	
Val	Tyr	Leu	Asn	Gly	Asp	Gly	Met	Gly	Lys	Gly	Thr	His	Leu	Ser	Leu		
			460					465					470				
TTT	TTT	GTC	ATC	ATG	CGT	GGA	GAA	TAT	GAT	GCC	CTG	CTT	CCT	TGG	CCG	1674	
Phe	Phe	Val	Ile	Met	Arg	Gly	Glu	Tyr	Asp	Ala	Leu	Leu	Pro	Trp	Pro		
		475					480					485					
TTT	AAG	CAG	AAA	GTG	ACA	CTC	ATG	CTG	ATG	GAT	CAG	GGG	TCC	TCT	CGA	1722	
Phe	Lys	Gln	Lys	Val	Thr	Leu	Met	Leu	Met	Asp	Gln	Gly	Ser	Ser	Arg		
	490					495					500						

CGT CAT TTG GGA GAT GCA TTC AAG CCC GAC CCC AAC AGC AGC AGC TTC	1770
Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe	
505 510 515 520	
AAG AAG CCC ACT GGA GAG ATG AAT ATC GCC TCT GGC TGC CCA GTC TTT	1818
Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe	
525 530 535	
GTG GCC CAA ACT GTT CTA GAA AAT GGG ACA TAT ATT AAA GAT GAT ACA	1866
Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr	
540 545 550	
ATT TTT ATT AAA GTC ATA GTG GAT ACT TCG GAT CTG CCC GAT CCC	1911
Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro	
555 560 565	
CGTGGGAGGT GGATTTAGCA GAAGGCAACT CCTCTGGGGG ATTTGAACCG	1971
GTCTGTCTTC ACTGAGGTCC TCGCGCTCAG AAAAGGACCT TGTGAGACGG AGGAAGCGGC	2031
AGAAGGCGGA CGCGTGCCGG CGGGAGGAGC CACGCGAGAG CACACCTGAC ACGTTTTATA	2091
ATAGACTAGC CACACTTCAC TCTGAAGAAT TATTTATCCT TCAACAAGAT AAATATTGCT	2151
GTCAGAGAAG GTTTTCATTT TCATTTTAA AGATCTAGTT AATTAAGGTG GAAAACATAT	2211
ATGCTAAACA AAAGAAACAT GATTTTCTT CCTTAAACTT GAACACCAAA AAAACACACA	2271
CACACACACA CGTGGGGATA GCTGGACATG TCAGCATGTT AAGTAAAAGG AGAATTTATG	2331
AAATAGTA	2339

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn	
1 5 10 15	
Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe	
20 25 30	
Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu	
35 40 45	
Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys	
50 55 60	
Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu	
65 70 75 80	
Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val	
85 90 95	
Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala	
100 105 110	

Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu  
 115 120 125  
 Met Leu Gly His Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu  
 130 135 140  
 Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp  
 145 150 155 160  
 Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys  
 165 170 175  
 Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu  
 180 185 190  
 Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser  
 195 200 205  
 Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys  
 210 215 220  
 Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe  
 225 230 235 240  
 Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val  
 245 250 255  
 Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys  
 260 265 270  
 Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln  
 275 280 285  
 Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln  
 290 295 300  
 Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg  
 305 310 315 320  
 Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile  
 325 330 335  
 Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser  
 340 345 350  
 Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys  
 355 360 365  
 Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu  
 370 375 380  
 Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp  
 385 390 395 400  
 Met Asp Leu Gly Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val  
 405 410 415  
 Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val  
 420 425 430  
 Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr  
 435 440 445

Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met  
 450 455 460

Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu  
 465 470 475 480

Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met  
 485 490 495

Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys  
 500 505 510

Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn  
 515 520 525

Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn  
 530 535 540

Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp  
 545 550 555 560

Thr Ser Asp Leu Pro Asp Pro )  
 565

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys  
 1 5 10 15

Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu  
 20 25 30

Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val  
 35 40 45

Lys

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Lys Tyr Leu Cys Ser Ala Cys Lys Asn Ile Leu Arg Arg Pro Phe  
 1 5 10 15

Gln Ala Gln Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Thr Ser Ile  
 20 25 30

Leu Ser Ser Gly Pro Gln Asn Cys Ala Ala Cys Val Tyr Glu Gly Leu  
35 40 45

Tyr Glu  
50

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Ser Ile Ser Cys Gln Ile Cys Glu His Ile Leu Ala Asp Pro Val  
1 5 10 15  
 Glu Thr Asn Cys Lys His Val Phe Cys Arg Val Cys Ile Leu Arg Cys  
20 25 30  
 Leu Lys Val Met Gly Ser Tyr Cys Pro Ser Cys Arg Tyr Pro Cys Phe  
35 40 45  
 Pro

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Glu Leu Met Cys Pro Ile Cys Leu Asp Met Leu Lys Asn Thr Met  
1 5 10 15  
 Thr Thr Lys Glu Cys Leu His Arg Phe Cys Ser Asp Cys Ile Val Thr  
20 25 30  
 Ala Leu Arg Ser Gly Asn Lys Glu Cys Pro Thr Cys Arg Lys Lys Leu  
35 40 45  
 Val Ser  
50

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 49 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Glu Val Thr Cys Pro Ile Cys Leu Asp Pro Phe Val Glu Pro Val  
 1 5 10 15  
 Ser Ile Glu Cys Gly His Ser Phe Cys Gln Glu Cys Ile Ser Gln Val  
 20 25 30  
 Gly Lys Gly Gly Gly Ser Val Cys Pro Val Cys Arg Gln Arg Phe Leu  
 35 40 45  
 Leu

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln Ala Phe Arg Cys His Val Cys Lys Asp Phe Tyr Asp Ser Pro Met  
 1 5 10 15  
 Leu Thr Ser Cys Asn His Thr Phe Cys Ser Leu Cys Ile Arg Arg Cys  
 20 25 30  
 Leu Ser Val Asp Ser Lys Cys Pro Leu Cys Arg Ala Thr Asp Gln Glu  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asn Lys Tyr Thr Cys Pro Ile Cys Phe Glu Phe Ile Tyr Lys Lys Gln  
 1 5 10 15  
 Ile Tyr Gln Cys Lys Ser Gly His His Ala Cys Lys Glu Cys Trp Glu  
 20 25 30  
 Lys Ser Leu Glu Thr Lys Lys Glu Cys Met Thr Cys Lys Ser Val Val  
 35 40 45  
 Asn Ser  
 50

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 179 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln	Met	Leu	Ser	Val	His	Asp	Ile	Arg	Leu	Ala	Asp	Met	Asp	Leu	Gly	1	5	10	15
Phe	Gln	Val	Leu	Glu	Thr	Ala	Ser	Tyr	Asn	Gly	Val	Leu	Ile	Trp	Lys	20	25	30	
Ile	Arg	Asp	Tyr	Lys	Arg	Arg	Lys	Gln	Glu	Ala	Val	Met	Gly	Lys	Thr	35	40	45	
Leu	Ser	Leu	Tyr	Ser	Gln	Pro	Phe	Tyr	Thr	Gly	Tyr	Phe	Gly	Tyr	Lys	50	55	60	
Met	Cys	Ala	Arg	Val	Tyr	Leu	Asn	Gly	Asp	Gly	Met	Gly	Lys	Gly	Thr	65	70	75	80
His	Leu	Ser	Leu	Phe	Phe	Val	Ile	Met	Arg	Gly	Glu	Tyr	Asp	Ala	Leu	85	90	95	
Leu	Pro	Trp	Pro	Phe	Lys	Gln	Lys	Val	Thr	Leu	Met	Leu	Met	Asp	Gln	100	105	110	
Gly	Ser	Ser	Arg	Arg	His	Leu	Gly	Asp	Ala	Phe	Lys	Pro	Asp	Pro	Asn	115	120	125	
Ser	Ser	Ser	Phe	Lys	Lys	Pro	Thr	Gly	Glu	Met	Asn	Ile	Ala	Ser	Gly	130	135	140	
Cys	Pro	Val	Phe	Val	Ala	Gln	Thr	Val	Leu	Glu	Asn	Gly	Thr	Tyr	Ile	145	150	155	160
Lys	Asp	Asp	Thr	Ile	Phe	Ile	Lys	Val	Ile	Val	Asp	Thr	Ser	Asp	Leu	165	170	175	
Pro Asp Pro																			

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg	Ser	Ile	Gly	Leu	Lys	Asp	Leu	Ala	Met	Ala	Asp	Leu	Glu	Gln	Lys	1	5	10	15
Val	Ser	Glu	Leu	Glu	Val	Ser	Thr	Tyr	Asp	Gly	Val	Phe	Ile	Trp	Lys	20	25	30	
Ile	Ser	Asp	Phe	Thr	Arg	Lys	Arg	Gln	Glu	Ala	Val	Ala	Gly	Arg	Thr	35	40	45	
Pro	Ala	Ile	Phe	Ser	Pro	Ala	Phe	Tyr	Thr	Ser	Arg	Tyr	Gly	Tyr	Lys	50	55	60	

Met	Cys	Leu	Arg	Val	Tyr	Leu	Asn	Gly	Asp	Gly	Thr	Gly	Arg	Gly	Thr
65					70					75					80
His	Leu	Ser	Leu	Phe	Phe	Val	Val	Met	Lys	Gly	Pro	Asn	Asp	Ala	Leu
				85					90					95	
Leu	Gln	Trp	Pro	Phe	Asn	Gln	Lys	Val	Thr	Leu	Met	Leu	Leu	Asp	His
			100					105					110		
Asn	Asn	Arg	Glu	His	Val	Ile	Asp	Ala	Phe	Arg	Pro	Asp	Val	Thr	Ser
		115					120					125			
Ser	Ser	Phe	Gln	Arg	Pro	Val	Ser	Asp	Met	Asn	Ile	Ala	Ser	Gly	Cys
	130					135					140				
Pro	Leu	Phe	Cys	Pro	Val	Ser	Lys	Met	Glu	Ala	Lys	Asn	Ser	Tyr	Val
145					150					155					160
Arg	Asp	Asp	Ala	Ile	Phe	Ile	Lys	Ala	Ile	Val	Asp	Leu	Thr	Gly	Leu
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gln	Thr	Leu	Ala	Gln	Lys	Asp	Gln	Val	Leu	Gly	Lys	Leu	Glu	His	Ser
1				5					10					15	
Leu	Arg	Leu	Met	Glu	Glu	Ala	Ser	Phe	Asp	Gly	Thr	Phe	Leu	Trp	Lys
			20					25					30		
Ile	Thr	Asn	Val	Thr	Lys	Arg	Cys	His	Glu	Ser	Val	Cys	Gly	Arg	Thr
		35					40					45			
Val	Ser	Leu	Phe	Ser	Pro	Ala	Phe	Tyr	Thr	Ala	Lys	Tyr	Gly	Tyr	Lys
	50					55					60				
Leu	Cys	Leu	Arg	Leu	Tyr	Leu	Asn	Gly	Asp	Gly	Ser	Gly	Lys	Lys	Thr
65					70					75					80
His	Leu	Ser	Leu	Phe	Ile	Val	Ile	Met	Arg	Gly	Glu	Tyr	Asp	Ala	Leu
				85					90					95	
Leu	Pro	Trp	Pro	Phe	Arg	Asn	Lys	Val	Thr	Phe	Met	Leu	Leu	Asp	Gln
			100					105					110		
Asn	Asn	Arg	Glu	His	Ala	Ile	Asp	Ala	Phe	Arg	Pro	Asp	Leu	Ser	Ser
		115					120					125			
Ala	Ser	Phe	Gln	Arg	Pro	Gln	Ser	Glu	Thr	Asn	Val	Ala	Ser	Gly	Cys
	130					135					140				
Pro	Leu	Phe	Phe	Pro	Leu	Ser	Lys	Leu	Gln	Ser	Pro	Lys	His	Ala	Tyr
145					150					155					160

Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val Asp Thr Ser Ala  
165 170 175